CLAIMS

1. A method for detecting genetic variation or polymorphism, i.e. a mutation, in a catalase gene comprising the steps of:

   a) providing a biological sample taken from a subject to be tested,

   b) detecting the presence or absence of a variant genotype of the catalase gene in the biological sample, the presence of a variant catalase genotype indicating an increased risk or a susceptibility to cancer, especially colon and rectal cancer, cancer death, coronary heart disease (CHD), and/or cerebrovascular stroke in said subject.

2. The method according to claim 1, wherein said variant genotype of the catalase gene is a homo- or heterozygote form of the mutation.

3. The method according to claim 1, wherein the detection step is a DNA-assay.

4. The method according to claim 1, wherein the detection step is carried out using a gene or DNA chip, microarray, strip, panel or similar combination of more than one genes, mutations, catalase RNA expressions or catalase concentration or activity to be assayed.

5. The method according to claim 1, wherein the allelic pattern is determined using polymerase chain reaction.

6. The method according to claim 1, wherein the biological sample is a blood sample or buccal swab sample.

7. The method according to claim 1, wherein the detection step is based on a capturing probe.

8. The method according to claim 1, wherein said method is used for determining whether a subject will benefit from treatment with a drug, nutrient or other therapy enhancing catalase production, levels or activity or inhibiting catalase catabolism or elimination in the subject.

9. The method according to claim 1, wherein said method is used for determining whether a subject will be at increased risk of adverse effects or reactions if catalase antagonists are administered to a subject.

10. The method according to claim 1, further comprising a step of selecting a subject with a catalase gene sequence reducing the expression, production or levels of catalase enzyme for clinical drug trials testing the cancer, coronary heart disease and/or stroke preventing effects of compounds.

11. The method according to claim 1, wherein the detected mutation is -262 C>T of 5'UTR of the catalase gene.

12. The method according to claim 1, wherein the detected mutation is Exon 8 Leu316Pro (T>C) of the catalase gene.

13. The method according to claim 1, wherein the detected mutation is Exon 9 Asp389Asp (C>T) of the catalase gene.

14. The method according to claim 1, further comprising a step of combining information concerning age, smoking, cancer history, leukocytes, drug for high cholesterol, serum ferritin, serum vitamin E, existing IHD disease, diabetes mellitus type 2, and retinol intake, drug for hypertension, adulthood socio-economic status (SES), HT, ischemic heart disease in family, plasma fibrinogen, mercury from hair and serum triglycerides in blood of the subject with the results from step b) of the method for confirming the indication obtained from said step.

15. The method according to preceding claims further comprising a step of calculating the probability of cancer, cancer death, coronary heart disease (CHD), and/or cerebrovascular stroke using a logistic regression equation as follows: Probability of a condition = $[1+e^{-(a+\Sigma (bi * Xi))}]^{-1}$, where e is Napier's constant, X_i's are variables related to the cancer or cancer deaths, b_i's are coefficient of these variables in the logistic function, and a is the constant term.

16. The method according to claim 15, wherein a and b_i's are determined in the population in which the method is to be used.

17. The method according to claim 15, wherein Xi's are selected among the variables that have been measured in the population in which the method is to be used.

18. The method according to claim 15, wherein b_i are between the values of –20 and 20

19. The method according to claim 15, wherein X_i's are between –99999 and 99999.

20. The method according to claim 15, wherein i are between the values 0 (none) and 100,000.

21. The method according to claim 15, wherein subject's short term, median term, and/or long term risk of cancer, CHD, and/or stroke is predicted.

22. A kit for detecting genetic variation or polymorphism, i.e. a mutation, in the catalase gene for the determination of a risk of cancer, especially colon and rectal cancer, cancer deaths, CHD, and/or stroke, in a subject, comprising means for catalase gene allele detection, and optionally software to interpret the results of the determination.

23. The kit according to claim 22 comprising a capturing nucleic acid probe specifically binding to the variant genotype as defined in any one of claims 11-13.

24. The kit according to claim 22 or 23, comprising a DNA chip, microarray, DNA strip, DNA panel or real-time PCR based tests.

25. The kit according to any one of claims 22-24, comprising a questionnaire for obtaining patient information concerning age, smoking, cancer history, drug for high cholesterol, existing IHD disease, diabetes mellitus type 2, and retinol intake, drug for hypertension, adulthood socio-economic status (SES), HT, and ischemic heart disease in family.

26. An isolated variant nucleic acid encoding catalase protein, said nucleic acid comprising CAT Exon 8 Leu316Pro (T>C) mutation.

27. The nucleic acid according to claim 26 further comprising CAT –262 C>T 5'UTR and/or CAT Exon 9 Asp389Asp (C>T) mutation.

28. The nucleic acid according to claim 26 or 27, wherein said nucleic acid is a genomic nucleotide sequence.

29. The nucleic acid according to claim 28, wherein said nucleic acid is cDNA.

30. The nucleic acid according to claim 26 comprising an RNA sequence.

31. The nucleic acid according to 26 having the nucleic acid sequence set forth in SEQ ID NO:26.

32. A capturing probe specifically binding to the nucleic acid according to claim 26.

33. The capturing probe according to claim 32, which comprises a single strand of the cDNA according to claim 29.

34. The capturing probe according to claim 32 or 33, which is specifically binding to variant catalase nucleic acid according to claim 26, but do not bind non-variant catalase.

35. A method for determining the presence or absence of a nucleic acid as defined in claim 26 in a biological sample comprising the steps of:

a) treating said sample to obtain single stranded target nucleic acid, or if the target nucleic acid are already single stranded, directly employing step (b);

b) contacting said target nucleic acid with a capturing nucleic acid probe and a detector nucleic acid probe;

c) detecting the complex of capturing probe, target nucleic acid and detector probe.

36. The method according to claim 35, wherein the capturing nucleic acid probe is attached or capable of attaching to a solid phase, and comprises the cDNA sequence according to claim 29, and wherein a detected signal from the solid phase is an indication of the presence in the sample of a nucleic acid as defined in claim 26.

37. The method according to claim 35, wherein the capturing nucleic acid probe is attached or capable of attaching to a solid phase, and comprises a cDNA corresponding to the gene coding a wild-type catalase protein, and wherein a detected signal from the solid phase is an indication of the absence of the nucleic acid as defined in claim 26 in the sample.

38. A transgenic animal which carries a human DNA sequence comprising a nucleotide sequence encoding a variant catalase nucleic acid as defined in claim 26.

39. RNA interference methods and models involving a variant nucleotide sequence encoding a variant catalase nucleic acid as defined in claim 26.

40. A method for targeting the treatment of cancer, CHD, and/or stroke by determining the pattern of alleles encoding a catalase, i.e. by determining if said subject's genotype of the catalase is of the variant type, comprising the steps presented in claim 1, and treating a subject of the variant genotype with a drug affecting catalase production or metabolism of the subject.

41. The method according to claim 40, wherein the variant genotype is as defined in any one of claims 11-13.

42. The method according to claim 40 or 41, wherein said variant genotype of the catalase is a homozygote or heterozygote form of mutation.

43. A method for treating a human or animal suffering from cancer, CHD or cerebrovascular stroke or for preventing said disease, said method comprising a therapy enhancing catalase availability, production or concentration of the human subject or animal.

44. The method of claim 43, wherein said animal is a mammal.

45. A method for treating vascular complications of cancer, CHD or stroke, said method comprising a step of enhancing catalase availability, production or concentration in the circulation of a human subject or animal.

46. The method according to any one of claims 43 - 45, said method comprising administering to a subject a compound enhancing catalase enzyme availability, production or concentration of the subject.

47. The method according to any one of claims 43 - 45, wherein the said method of treating is a dietary treatment or a vaccination.

48. The method according to any one of claims 43 - 45, wherein said therapy is gene therapy or gene transfer.

49. The method according to claim 48, wherein said therapy comprises the transfer of the non-variant catalase gene or fragment or derivative thereof.